

What is claimed is:

1. DNA comprising a promoter sequence and associated coding sequence wherein the promoter sequence drives expression of the coding sequence specifically in the tapetum, endothecium and connective tissues of anthers but not in microspores or pollen, and wherein expression of the coding sequence starts at the tetrad stage and reaches a maximum level at the vacuolated pollen stage.
2. The DNA according to claim 1, wherein the sequence comprises a nucleotide sequence having 50% or more sequence identity with the sequence shown in SEQ ID NO:1.
3. The DNA according to claim 1, wherein the sequence comprises the nucleotide sequence shown in SEQ ID NO:1.
4. The DNA according to any one of claims 1 to 3, wherein the coding sequence is in antisense orientation.
5. The DNA according to any one of claims 1 to 3, wherein the coding sequence encodes a polypeptide which will disrupt formation of viable pollen when expressed in the anther cells.
6. The DNA according to claim 5, wherein the coding sequence encodes a polypeptide selected from the group consisting of RNase, DTA, TURF-13, pectate lyase, gin recombinase, iaaL and cytA toxin.
7. A DNA sequence having more than 80% sequence identity in the consecutive 30 bases of any sites of SEQ ID NO:1.
8. DNA comprising a promoter sequence capable of driving expression of an associated coding sequence specifically in the tapetum, endothecium and connective tissue of anthers but not in microspores or pollen, wherein expression of the coding sequence starts at the tetrad stage and reaches a maximum level at the vacuolated pollen stage.
9. The DNA of claim 8, wherein the promoter sequence has 50% or more sequence identity with the nucleotide sequence of SEQ ID NO:3.

10. The DNA of claim 9, wherein the promoter sequence has the nucleotide sequence shown in SEQ ID NO:3.

11. The DNA according to any one of claims 1 to 10, wherein the promoter sequence comprises an additional sequence that can be operatively linked to a coding sequence of interest.

12. The DNA according to claim 11, wherein the additional sequence comprises a sequence having 50% or more sequence identity with SEQ ID NO:10.

13. The DNA according to claim 11, wherein the additional sequence comprises SEQ ID NO:10.

14. The DNA according to claims 9 to 13, wherein the promoter sequence and additional sequence have 50% or more sequence identity with the respective sequences of SEQ ID NO:2.

15. The DNA according to claims 9 to 13, wherein the promoter sequence and additional sequence are characterized by the nucleotide sequence of SEQ ID NO:2.

16. The DNA according to claim 15, wherein the promoter comprises a fragment obtainable from SEQ ID NO:2.

17. DNA comprising an open reading frame encoding a protein characterized by an amino acid sequence having 50% or more sequence identity with SEQ ID NO:4.

18. The DNA according to claim 17, wherein the open reading frame encodes a protein characterized by the amino acid sequence of SEQ ID NO:4.

19. The DNA according to any one of claims 17 or 18 characterized by SEQ ID NO:7.

20. An expression vector comprising a first expression cassette comprising a DNA of any one of claims 1 to 19 for expression in a host organism such as a microorganism or a plant and, optionally, a second expression cassette comprising a gene of interest.

21. The protein encoded by the open reading frame of any one of claims 17 to 19.

22. A transgenic plant and the sexual and/or asexual progeny thereof, which has been transformed with a DNA sequence according to any one of claims 1 to 19.

23. A transgenic, male-sterile plant which has been transformed with a DNA sequence according to any one of claims 1 to 19.

24. A transgenic plant according to claims 22 or 23, wherein the plant is rice, wheat, maize, *Sorghum bicolor* or orchardgrass.

25. A process for the production of a transgenic plant comprising a DNA comprising a promoter sequence and associated coding sequence wherein the promoter sequence drives expression of the coding sequence specifically in the tapetum, endothecium and connective tissues of anthers but not in microspores or pollen, and wherein expression of the coding sequence starts at the tetrad stage and reaches a maximum level at the vacuolated pollen stage.

26. A process according to claim 25, wherein the plant is rice, wheat, maize, *Sorghum bicolor* or orchardgrass.